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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|---|---|---|---|---|
| 10/548,748 | 09/08/2005 | Markus Frank | 12810-00137-US | 1250 |

23416 7590 02/07/2008

CONNOLLY BOVE LODGE & HUTZ, LLP
P O BOX 2207
WILMINGTON, DE 19899

| EXAMINER | |
|---|---|
| IBRAHIM, MEDINA AHMED | |

| ART UNIT | PAPER NUMBER |
|---|---|
| 1638 | |

| MAIL DATE | DELIVERY MODE |
|---|---|
| 02/07/2008 | PAPER |

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

| Office Action Summary | Application No. | Applicant(s) | |
|---|---|---|---|
| | 10/548,748 | FRANK ET AL. | |
| | Examiner | Art Unit | |
| | Medina A. Ibrahim | 1638 | |

*-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --*

**Period for Reply**

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

**Status**

1)☒ Responsive to communication(s) filed on *01 November 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

**Disposition of Claims**

4)☒ Claim(s) *1-3,6-17,19,20 and 22-25* is/are pending in the application.

4a) Of the above claim(s) *12 and 13* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-3,6-11,14-17,19,20 and 22-25* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

**Application Papers**

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

**Priority under 35 U.S.C. § 119**

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

**Attachment(s)**

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☒ Other: *aligment of sequences*.

## DETAILED ACTION

1. The text of those sections of Title 35, U.S. Code not included in this action can be found in a prior Office action.

2. Applicant's response filed 11/01/07 in reply to the Office action of 05/01/07 has been entered. The sequence listing has been entered. Claims 1, 6-9, 14-17, 19-20 are amended. Claims 4-5, 18, and 21 are cancelled. New claims 22-24 are added. Therefore, claims 1-3, 6-17, 19-20, and 22-25 are pending.

This application contains claims 12-13, drawn to an invention nonelected with traverse in the reply filed on 03/16/07. A complete reply to the final rejection must include cancellation of nonelected claims or other appropriate action (37 CFR 1.144) See MPEP § 821.01.

3. Claims 1-3, 6-11, 14-17, 19-20, and 22-25 are examined.

4. All previous objections and rejections not set forth below have been withdrawn in view of Applicant's amendment to the claims and/or upon further consideration.

### *Claim Rejections - 35 USC § 112*

Claims 1-3, 6-11, 14-17, 19-20 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a method of generating resistance in a plant to at least at least one plant pathogen by transforming the plant with an isolated nucleic acid encoding the unmodified Bax protein of SEQ ID NO: 2 under the control of a desired promoter, and a recombinant vector/cassette comprising said nucleic acid, does not reasonably provide enablement for a method that employs an isolated nucleic acid encoding a polypeptide having as low as 70% sequence identity to increase

resistance to all biotic and abiotic stresses in a transgenic plant or a recombinant vector/cassette comprising said nucleic acid. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and or use the invention commensurate in scope with these claims. This rejection is repeated for the reasons of record as set forth in the last Office action of 05/01/07. Applicant's arguments filed 11/01/07 have been fully considered but are not deemed persuasive.

Applicant's asserts that the claims are amended to recite a nucleic acid sequence having at least 70% to SEQ ID NO: 2 and require that the increased BI1 function or amount is achieved through transformation. Applicant also asserts that resistance to biotic and all abiotic stresses can be improved by the claimed method. Applicant argues that the instant specification describes motifs which are highly conserved between various BI1 proteins of different sources, and that one skilled in the art can easily determine mutations that would not impair the protein function using the sequence alignment shown in Figures 1 and 6 (response, pp. 13-14).

These arguments have been considered but are not persuasive because Applicant has not shown that sequences having as low as 70% identity to SEQ ID NO: 2 can increase resistance to exemplified or non exemplified stress. Applicant's has not taught which region in the functional domains would tolerate modifications. Lazar et al (1988, cited in the last Office action) teach that the conservative substitution of glutamic acid for aspartic acid at position 47 reduced biological function of transforming growth factor alpha, while "nonconservative" substitutions with alanine or asparagine had no

effect (see at least the Abstract). There is also a complete lack of guidance in the specification and in the prior art as to how and where the disclosed sequences or sequences having BI1 protein activity can be modified while retaining the desired activity. Given this highly unpredictable areas and lack of sufficient guidance in the specification, one skilled in the art would have to proceed with undue trial and error experimentation to screen through a vast number of polynucleotides encoding proteins with multiple of amino acid modifications to identify those having the functional activity of the protein sequence SEQ ID NO: 2.

*Genentech Inc. v. Novo Nordisk A/S*, 108 F.3d 1361, 1366, 42 USPQ2d 1001, 1005 (Fed. Cir. 1997) states. .... It is the specification, not the knowledge of one skilled in the art, that must supply the novel aspects of an invention in order to constitute adequate enablement". The *Genentech* court also held that [w]hile every aspect of a generic claim certainly need not have been carried out by an inventor, or exemplified in the specification, reasonable detail must be provided in order to enable members of the public to understand and carry out the invention". Id. In this case, as in *Genentech*, the specification does not provide the "reasonable detail .....to enable members of the public to understand and carry out the invention as broadly claimed".

See also, *Amgen Inc. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ 2d 1016 at 1027 (Fed. Cir. 1991) where the court held that the disclosure of a few gene sequences did not enable claims broadly drawn to any analog thereof. See also *In re Fisher*, 427 F.2d 833, 839, 166 USPQ 18, 24 (CCPA 1970) where it states " the scope of enablement must bear a "reasonable correlation" to the scope of the claims. In the

instant case, the scope of the claims does not reasonably correlate to the scope of enablement.

Also, Applicant's arguments that the resistance to all abiotic stresses can be improved with exemplified or non-exemplified sequences and claimed methods are not found persuasive. The instant specification discloses transgenic plants expressing BI1 sequences having resistance to various plant fungal diseases such as powdery mildew, leaf rust, diseases caused by fungal pathogens *Bipolars sorokiniana, Magnoprthe grisea and Fusarium spp.* Applicant has not disclosed a single transgenic plant having resistance to heat, cold, drought, increased humidity, UV radiation or chemical stresses as a result of expressing exemplified or non-exemplified sequences BI1 protein.

As stated in the last Office action, Mittler et al (Plant Cell (1996) 8:1991-2001) teach expression of a BaxI1 gene in transgenic plants didn't result in resistance to bacterial and viral induced cell death (see at least Abstract on page 19991, and Discussion pages 1996-1998). Therefore, Applicant provides no evidence to support the conclusion that resistance to all abiotic stresses can be improved using BI1 sequences having as low as 70% sequence identity to SEQ ID NO: 2.

Therefore, given the lack of guidance in the specification and in the prior art; the unpredictability inherent in transforming plants for universal disease resistance as evidenced by Ryals et al (1996) and Mittler et al (1996); and the nature of the invention as discussed above, the claimed invention cannot be practiced throughout the broad scope, therefore, the invention is not enabled.

***Claim Rejections - 35 USC § 102***

1. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

5. Claims 1-2, 6-11, 14-17, 19-20 are rejected under 35 U.S.C. 102(a) as being anticipated by Simmons et al (WO 2002101079A2, Applicant's IDS).

The claims are drawn to a method of increasing resistance to biotic or abiotic stresses by transforming a plant with a nucleic acid encoding a BII having at least 70% sequence identity to SEQ ID NO: 2 to increase the amount or the function of bax1 inhibitor protein with the proviso that expression in leaf epidermis in said plant remains unchanged or reduced, and selecting the plant that exhibit increased resistance to at least one biotic or abiotic stress; said method further comprising stably transforming a plant cell with said nucleic acid under the control of a tuber or root specific promoter, and regenerating a stably transformed plant; a recombinant expression cassette/vector comprising said nucleic acid operably linked to a heterologous tissue-specific promoter, said promoter having essentially no activity in the leaf epidermis, said promoter is mesophyll, root or tuber -specific promoter; and a recombinant plant comprising said expression cassette/vector. The claims are also drawn to said recombinant plant additionally having a mlo resistant phenotype.

Simmons et al teach a method of increasing resistance to abiotic and biotic stresses in a plant by transforming a plant a recombinant expression cassette comprising a nucleic acid encoding a Bax inhibitor I protein having at least 85% sequence identity to SEQ ID NO: 2 (see attached alignment of sequences) under the control of a root-specific, fruit-specific, seed-specific or flower-specific promoters (pages 7-8; 19-20; see page 8, parag# 0117). The cited reference also teaches various methods of transforming a plant cell, selecting transformed cells, and regenerating a stably transformed plant from the plant cell; plants to be transformed include monocots and dicots such maize, soybean, tobacco, potato, tomato, sunflower, canola, wheat, rice, and barley (pages 35-40; and Examples 5-12 and 14-15). Pathogens include fungal pathogens such as Altemaria, Botrytis; Erysiphe, Rhizopus oryzae, Rhizopus, Puccinia helianthi, Verticillium, Erwinia, Cephalosporium, Phytophthora and Fusarium (pages 44-46). The cited further teaches that either heterologous or non-heterologous promoters can be used with BI1 nucleic acids in expression cassettes to drive expression of antisense nucleic acids to reduce, increase, or alter concentration of the BI1 proteins in a desired tissue (page 20, lines 17-22). The transgenic plants expressing BI1 protein in the roots, flowers or seeds would have no BI1 activity in leaf epidermis. Therefore, the plant would inherently possess mlo resistant phenotype. Therefore, Simmons et al teach all claim limitations.

***Claim Rejections - 35 USC § 103***

2. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

3. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

4. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

5. Claims 1-3, 6-11, 14-17, 19-20, and 22-25 are rejected under 35 U.S.C. 103(a) as being unpatentable over Simmons et al ( WO 2002101079A2, Applicant's IDS) in view of Huckelhoven et al (Plant Mol. Biol. (2001) 47 (6):739-748).

The claims are drawn to a method of increasing resistance to biotic or abiotic stresses by transforming a plant with a nucleic acid encoding a BII having at least 70%, 90%, or 95% sequence identity to SEQ ID NO: 2 to increase the amount or the function of bax1 inhibitor protein with the proviso that expression in leaf epidermis in said plant remains unchanged or reduced, and selecting the plant that exhibit increased resistance to at least one biotic or abiotic stress; said method further comprising stably transforming a plant cell with said nucleic acid under the control of a tuber or root specific promoter, and regenerating a stably transformed plant; a recombinant expression cassette/vector comprising said nucleic acid operably linked to a heterologous tissue-specific promoter, said promoter having essentially no activity in the leaf epidermis, said promoter is mesophyll, root or tuber -specific promoter; and a recombinant plant comprising said expression cassette/vector. The claims are also drawn to said recombinant plant additionally having a mlo resistant phenotype.

6. Simmons et al teach a method of increasing resistance to abiotic and biotic stresses in a plant by transforming the plant a recombinant expression cassette comprising a nucleic acid encoding a bax inhibitor I protein operably linked to a root-specific, fruit-specific, seed-specific or flower-specific promoter, and transgenic monocot and dicot plants as discussed above.

7. Simmons et al do not explicitly teach the use of nucleic acid encoding a BaxI1 protein having at least 95% sequence identity to SEQ ID NO: 2, or teach resistance to stress factor that is necrotrophic or hemibiotrophic pathogen.

8. Huchelhoven et al teach a nucleic acid encoding a BaxI1 protein that is 100% identical to SEQ ID NO:2 (see attached alignment of sequences), its role in barley defense against *Bgh*, its functional relationship with the barley mlo resistant gene, and suggest the barley Bax inhibitor may have role in restricting the spread of cell death in HR tissues after fungal attack. The cited reference further suggests tissue-specific expression of the Bax I1 in barley cells inoculated with Bgh is carried out (see the whole document).

9. Therefore, it would have been obvious to one of ordinary skill in the art at the time the invention was made to use the method of transforming a plant with a nucleic acid encoding a BaxI1 inhibitor under the control of a tissue-specific promoter to induce resistance against a plant pathogen as taught by Simmons et al, and to modify that method by incorporating any other known BaxI1 nucleic acid such as the barley BaxI1 nucleic acid taught by Huchelhoven et al. One would have a reasonable expectation of success as taught by Simmons et al. One would have been motivated to use the barley BaxI1 sequence, given that it is well characterized in its ability to suppress cell death in tissue-specific manner as taught by Huchelhoven et al, and given the problem of abiotic and abiotic stresses in crop production as taught by Simmons et al. One of ordinary skill in the art would expect that expression of the barley BaxI1 nucleic acid in a transgenic plant would increase or induce resistance against any necrotrophic or hemibiotrophic plant fungal pathogen as taught by Huchelhoven et al. Therefore, the claimed invention as whole was clearly a *prima facie* obvious.

Remarks

10. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure. Glazebrooke et al (WO 2003000906-A2, published 01/03/2003). Glazebrooke et al teach an isolated polynucleotide encoding a BaxI1 protein having at least 89% sequence identity to SEQ ID NO: 2 (see attached alignment of sequences) and methods of its use in transgenic plants to induce resistance.

No claim is allowed.

***Contact Information***

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Medina A. Ibrahim whose telephone number is (571) 272-0797. The Examiner can normally be reached Monday -Thursday from 8:00AM to 5:30PM and every other Friday from 9:00AM to 5:00 PM . The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

If attempts to reach the Examiner by telephone are unsuccessful, the Examiner's supervisor, Anne Marie Grunberg, can be reached at (571) 272-0975.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

2/4/08
Mai

MEDINA A. IBRAHIM
PRIMARY EXAMINER

<!--StartFragment-->RESULT 11
AAD54462
ID  AAD54462 standard; cDNA; 1138 BP.
XX
AC  AAD54462;
XX
DT  17-JUN-2003  (first entry)
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KW  Bax inhibitor; BI; transgenic; plant; disease resistance; sterility;
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OS  Synthetic.
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XX
PD  19-DEC-2002.
XX
PF  11-JUN-2002; 2002WO-US019114.
XX
PR  12-JUN-2001; 2001US-0297478P.
XX
PA  (PION-) PIONEER HI-BRED INT INC.
XX
PI  Simmons CR, Gordon-Kamm WJ, Johal G, Acevedo PAN, Tao Y;
XX
DR  WPI; 2003-156968/15.
DR  P-PSDB; AAE35962.
XX
PT  New nucleic acid encoding a polypeptide that modulates Bax inhibitor
PT  activity, useful for identifying transgenic events or for improving
PT  disease resistance mechanisms in a plant.
XX
PS  Claim 1; Page 115-116; 117pp; English.
XX
CC  The invention relates to a nucleic acid encoding a polypeptide that
CC  modulate Bax inhibitor (BI) activity. Nucleic acid molecules of the
CC  invention are useful for improving transformation efficiency in plant
CC  cells compared to control plant cells, for identifying transgenic events,
CC  for improving disease resistance mechanisms in a plant, for affecting the
CC  architecture of plants or for increasing male sterility. The present

CC sequence is (maize) Zea mays (Zm) BI mutant cDNA
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SQ Sequence 1138 BP; 215 A; 351 C; 321 G; 251 T; 0 U; 0 Other;

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| Percent Similarity: | 90.6% | Conservative: | 26 |
| Best Local Similarity: | 80.5% | Mismatches: | 13 |
| Query Match: | 85.4% | Indels: | 11 |
| DB: | 8 | Gaps: | 2 |

US-10-548-748-2 (1-247) x AAD54462 (1-1138)

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Qy         31 GlnSerHisLeuLysLeuValTyrLeuThrLeuCysPheAlaLeuAlaSerSerAlaVal  50
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Qy        111 AspPheAspProSerIleLeuValThrGlyPheValGlyThrAlaIleAlaPheGlyCys  130
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Qy        230 LeuLysAsnAlaGlyAspLysSerGluAspLysLysLysArgLysArg 245
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<!--EndFragment-->

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AC  ADA48744;
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DT  20-NOV-2003  (first entry)
XX
DE  Rice protein conferring disease resistance in plants.
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KW  disease resistance; pathogen tolerance; plant pathogen; plant; rice.
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OS  Oryza sativa.
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XX
PD  03-JAN-2003.
XX
PF  21-JUN-2002; 2002WO-IB002453.
XX
PR  22-JUN-2001; 2001US-0300112P.
PR  26-SEP-2001; 2001US-0352277P.
PR  22-MAR-2002; 2002US-0366535P.
XX
PA  (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI  Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
PI  Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX
DR  WPI; 2003-184052/18.
DR  N-PSDB; ADA48743.
XX
PT  New polynucleotide comprising a plant nucleotide sequence having an open
PT  reading frame that encodes a polypeptide associated with disease
PT  resistance, useful for conferring resistance or tolerance to a plant
PT  pathogen.
XX
PS  Claim 10; SEQ ID NO 814; 299pp; English.
XX
CC  The invention relates to a novel isolated polynucleotide comprising a
CC  plant nucleotide sequence having an open reading frame that encodes a
CC  polypeptide associated with disease resistance or its fragment having
CC  substantially the same activity as the full-length polypeptide. The
CC  polynucleotide of the invention is useful for conferring resistance or
CC  tolerance to a plant pathogen. The present sequence represents a protein
CC  conferring disease resistance used in the invention.
XX
SQ  Sequence 249 AA;

Query Match 89.9%; Score 1127.5; DB 6; Length 249;
Best Local Similarity 87.9%; Pred. No. 2.3e-123;
Matches 218; Conservative 18; Mismatches 9; Indels 3; Gaps 1;

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Qy        118 VTGFVGTAIAFGCFSGAAIIAKRREYLYLGGLLSSGLSILLWLQFVTSIFGHSSGSFMFE 177
              || ||||||||||: |||:|||||||||||||||||||||||  ||||||:||||||
Db        121 VTAFVGTAIAFGCFTCAAIVAKRREYLYLGGLLSSGLSILLWLQFAASIFGHSTGSFMFE 180

Qy        178 VYFGLLIFLGYMVYDTQEIIERAHHGDMDYIKHALTLFTDFVAVLVRVLIIMLKNAGDKS 237
              |||||||||||||||||||||||||||||||||||||||||||||:|:|||||| |||
Db        181 VYFGLLIFLGYMVYDTQEIIERAHHGDMDYIKHALTLFTDFVAVLVRILVIMLKNASDKS 240

Qy        238 EDKKKRKR 245
              |:||::||
Db        241 EEKKRKKR 248
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<!--EndFragment-->

<!--StartFragment-->RESULT 8
ADA48743
ID   ADA48743 standard; DNA; 750 BP.
XX
AC   ADA48743;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Rice gene conferring disease resistance in plants.
XX
KW   disease resistance; pathogen tolerance; plant pathogen; ds; gene; plant.
XX
OS   Oryza sativa.
XX
PN   WO2003000906-A2.
XX
PD   03-JAN-2003.
XX
PF   21-JUN-2002; 2002WO-IB002453.
XX
PR   22-JUN-2001; 2001US-0300112P.
PR   26-SEP-2001; 2001US-0352277P.
PR   22-MAR-2002; 2002US-0366535P.
XX
PA   (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI   Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;
PI   Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX
DR   WPI; 2003-184052/18.
DR   P-PSDB; ADA48744.
XX
PT   New polynucleotide comprising a plant nucleotide sequence having an open
PT   reading frame that encodes a polypeptide associated with disease
PT   resistance, useful for conferring resistance or tolerance to a plant
PT   pathogen.
XX
PS   Claim 1; SEQ ID NO 813; 299pp; English.
XX
CC   The invention relates to a novel isolated polynucleotide comprising a
CC   plant nucleotide sequence having an open reading frame that encodes a
CC   polypeptide associated with disease resistance or its fragment having
CC   substantially the same activity as the full-length polypeptide. The
CC   polynucleotide of the invention is useful for conferring resistance or
CC   tolerance to a plant pathogen. The present sequence represents a gene
CC   conferring disease resistance used in the invention.
XX
SQ   Sequence 750 BP; 128 A; 212 C; 216 G; 194 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 4.82e-130 | Length: | 750 |
| Score: | 1127.50 | Matches: | 218 |
| Percent Similarity: | 95.2% | Conservative: | 18 |
| Best Local Similarity: | 87.9% | Mismatches: | 9 |
| Query Match: | 89.9% | Indels: | 3 |
| DB: | 9 | Gaps: | 1 |

US-10-548-748-2 (1-247) x ADA48743 (1-750)

```
Qy          1 MetAspAlaPheTyrSerThrSerSer---------AlaAlaAlaSerGlyTrpGlyHis 17
              |||||||||||||||||||||||||||         ||||||||||||||||||||:::
Db          1 ATGGACGCCTTCTACTCGACCTCGTCGGCGTACGGAGCGGCGGCGAGCGGCTGGGGCTAC 60

Qy         18 AspSerLeuLysAsnPheArgGlnIleSerProAlaValGlnSerHisLeuLysLeuVal 37
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GACTCGCTGAAGAACTTCCGCCAGATCTCCCCCGCCGTCCAGTCCCACCTCAAGCTCGTT 120

Qy         38 TyrLeuThrLeuCysPheAlaLeuAlaSerSerAlaValGlyAlaTyrLeuHisIleAla 57
              ||||||||||||||||   |||||||||:::|||||||||||||||||||||||:::|||
Db        121 TACCTGACACTATGCGTCGCCCTGGCTGCGTCGGCGGTGGGCGCATACCTGCACGTCGCC 180

Qy         58 LeuAsnIleGlyGlyMetLeuThrMetLeuAlaCysValGlyThrIleAlaTrpMetPhe 77
              ||||||||||||||||||||||||||||||   |||||||||:::|||||||||:::|||
Db        181 TTGAACATCGGCGGGATGTTGACTATGCTCGGGTGCGTGGGGAGCATCGCCTGGTTGTTC 240

Qy         78 SerValProValTyrGluGluArgLysArgPheGlyLeuLeuMetGlyAlaAlaLeuLeu 97
              ||||||||||||:::|||||||||||||||||||||:::|||:::   ||||||||||||
Db        241 TCGGTGCCTGTCTTTGAGGAGAGGAAGAGGTTTGGGATTCTCTTGGCCGCTGCCCTGCTG 300

Qy         98 GluGlyAlaSerValGlyProLeuIleGluLeuAlaIleAspPheAspProSerIleLeu 117
              ||||||||||||||||||||||||||:::||||||:::|||||||||   |||||||||
Db        301 GAAGGGGCTTCAGTTGGGCCTCTGATCAAGCTTGCTGTAGACTTTGACTCAAGCATTCTC 360

Qy        118 ValThrGlyPheValGlyThrAlaIleAlaPheGlyCysPheSerGlyAlaAlaIleIle 137
              ||||||   ||||||||||||||||||||||||||||:::   |||||||||:::
Db        361 GTAACAGCATTTGTTGGAACTGCCATTGCATTTGGGTGCTTCACTTGCGCTGCCATCGTT 420

Qy        138 AlaLysArgArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyLeuSerIleLeu 157
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCAAGCGTAGGGAGTACCTCTACCTTGGTGGTTTGCTCTCTTCTGGCCTCTCCATCCTG 480

Qy        158 LeuTrpLeuGlnPheValThrSerIlePheGlyHisSerSerGlySerPheMetPheGlu 177
              ||||||||||||||      ||||||||||||||:::||||||||||||||||||
Db        481 CTCTGGCTGCAGTTTGCCGCATCCATCTTTGGCCACTCCACCGGCAGCTTCATGTTTGAG 540

Qy        178 ValTyrPheGlyLeuLeuIlePheLeuGlyTyrMetValTyrAspThrGlnGluIleIle 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        541 GTTTACTTTGGCCTGTTGATCTTCCTGGGGTACATGGTGTATGACACGCAGGAGATCATC 600

Qy        198 GluArgAlaHisHisGlyAspMetAspTyrIleLysHisAlaLeuThrLeuPheThrAsp 217
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAGAGGGCTCACCACGGTGACATGGACTACATCAAGCACGCACTCACCCTCTTCACTGAC 660

Qy        218 PheValAlaValLeuValArgValLeuIleIleMetLeuLysAsnAlaGlyAspLysSer 237
              ||||||||||||||||||||:::|||:::|||||||||||||||||   |||||||||
Db        661 TTCGTGGCCGTCCTTGTCCGGATCCTCGTCATCATGCTCAAGAACGCGTCTGACAAGTCG 720

Qy        238 GluAspLysLysLysArgLysArg 245
              |||:::||||||:::::||||||
Db        721 GAGGAGAAGAAGAGGAAGAAGAGG 744
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<!--EndFragment-->

<!--StartFragment-->HVU290421 744 bp mRNA linear PLN 18-JAN-2002
DEFINITION Hordeum vulgare mRNA for BAX inhibitor 1 (pBI-1 gene).
ACCESSION AJ290421
VERSION AJ290421.1 GI:13940164
KEYWORDS BAX inhibitor 1; pBI-1 gene.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade; Pooideae; Triticeae; Hordeum.
REFERENCE 1
AUTHORS Huckelhoven,R., Dechert,C., Trujillo,M. and Kogel,K.H.
TITLE Differential expression of putative cell death regulator genes in near-isogenic, resistant and susceptible barley lines during interaction with the powdery mildew fungus
JOURNAL Plant Mol. Biol. 47 (6), 739-748 (2001)
PUBMED 11785935
REFERENCE 2 (bases 1 to 744)
AUTHORS Hueckelhoven,R.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-2001) Hueckelhoven R., Institute for Phytopatholgy and Applied Zoology, Justus-Liebig-University Giessen, Heinrich-Buff-Ring 26-32, 35392 Giessen, GERMANY
FEATURES Location/Qualifiers
source 1. .744
/organism="Hordeum vulgare subsp. vulgare"
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/cultivar="Pallas"
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/tissue_type="leaf"
/dev_stage="primary leaf"
gene 1. .744
/gene="pBI-1"
CDS 1. .744
/gene="pBI-1"
/function="putative cell death suppressor"
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/db_xref="GI:13940165"
/db_xref="UniProtKB/TrEMBL:Q93XL2"
/translation="MDAFYSTSSAAASGWGHDSLKNFRQISPAVQSHLKLVYLTLCFA
LASSAVGAYLHIALNIGGMLTMLACVGTIAWMFSVPVYEERKRFGLLMGAALLEGASV
GPLIELAIDFDPSILVTGFVGTAIAFGCFSGAAIIAKRREYLYLGGLLSSGLSILLWL
QFVTSIFGHSSGSFMFEVYFGLLIFLGYMVYDTQEIIERAHHGDMDYIKHALTLFTDF
VAVLVRVLIIMLKNAGDKSEDKKKRKRGS"
ORIGIN

Alignment Scores:

| | | | |
|---|---|---|---|
| Pred. No.: | 2.47e-142 | Length: | 744 |
| Score: | 1254.00 | Matches: | 247 |
| Percent Similarity: | 100.0% | Conservative: | 0 |
| Best Local Similarity: | 100.0% | Mismatches: | 0 |

Query Match: 100.0% Indels: 0
DB: 4 Gaps: 0

US-10-548-748-2 (1-247) x HVU290421 (1-744)

```
Qy          1 MetAspAlaPheTyrSerThrSerSerAlaAlaAlaSerGlyTrpGlyHisAspSerLeu 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGACGCCTTCTACTCGACCTCGTCGGCGGCGGCGAGCGGCTGGGGCCACGACTCCCTC 60

Qy         21 LysAsnPheArgGlnIleSerProAlaValGlnSerHisLeuLysLeuValTyrLeuThr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGAACTTCCGCCAGATCTCCCCCGCCGTGCAGTCCCACCTCAAGCTCGTTTACCTGACT 120

Qy         41 LeuCysPheAlaLeuAlaSerSerAlaValGlyAlaTyrLeuHisIleAlaLeuAsnIle 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTATGCTTTGCACTGGCCTCATCTGCCGTGGGTGCTTACCTACACATTGCCCTGAACATC 180

Qy         61 GlyGlyMetLeuThrMetLeuAlaCysValGlyThrIleAlaTrpMetPheSerValPro 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGCGGGATGCTGACAATGCTCGCTTGTGTCGGAACTATCGCCTGGATGTTCTCGGTGCCA 240

Qy         81 ValTyrGluGluArgLysArgPheGlyLeuLeuMetGlyAlaAlaLeuLeuGluGlyAla 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTCTATGAGGAGAGGAAGAGGTTTGGGCTGCTGATGGGTGCAGCCCTCCTGGAAGGGGCT 300

Qy        101 SerValGlyProLeuIleGluLeuAlaIleAspPheAspProSerIleLeuValThrGly 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCGGTTGGACCTCTGATTGAGCTTGCCATAGACTTTGACCCAAGCATCCTCGTGACAGGG 360

Qy        121 PheValGlyThrAlaIleAlaPheGlyCysPheSerGlyAlaAlaIleIleAlaLysArg 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTGTCGGAACCGCCATCGCCTTTGGGTGCTTCTCTGGCGCCGCCATCATCGCCAAGCGC 420

Qy        141 ArgGluTyrLeuTyrLeuGlyGlyLeuLeuSerSerGlyLeuSerIleLeuLeuTrpLeu 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGGAGTACCTGTACCTCGGTGGCCTGCTCTCGTCTGGCCTGTCGATCCTGCTCTGGCTG 480

Qy        161 GlnPheValThrSerIlePheGlyHisSerSerGlySerPheMetPheGluValTyrPhe 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGTTTGTCACGTCCATCTTTGGCCACTCCTCTGGCAGCTTCATGTTTGAGGTTTACTTT 540

Qy        181 GlyLeuLeuIlePheLeuGlyTyrMetValTyrAspThrGlnGluIleIleGluArgAla 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GGCCTGTTGATCTTCCTGGGGTACATGGTGTACGACACGCAGGAGATCATCGAGAGGGCG 600

Qy        201 HisHisGlyAspMetAspTyrIleLysHisAlaLeuThrLeuPheThrAspPheValAla 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CACCATGGCGACATGGACTACATCAAGCACGCCCTCACCCTCTTCACCGACTTTGTTGCC 660

Qy        221 ValLeuValArgValLeuIleIleMetLeuLysAsnAlaGlyAspLysSerGluAspLys 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCCTCGTCCGAGTCCTCATCATCATGCTCAAGAACGCAGGCGACAAGTCGGAGGACAAG 720

Qy        241 LysLysArgLysArgGlySer 247
```

```
                    ||||||||||||||||||||
Db          721 AAGAAGAGGAAGAGGGGGTCC 741
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<!--EndFragment-->